

## **IN THE CLAIMS**

Please amend claims 8-10 as follows:

1. (Previously Presented) A method for displaying gene expression patterns of multiple genes whose expressions change according to experiment cases, where a first axis represents the genes and a second axis represents gene expression status of the experiment cases, the method comprising the steps of:
  - designating a clustering-applied region along the second axis and a segment shorter than a width of the clustering-applied region along the second axis;
  - incrementally clustering the expression pattern data by the segment within the clustering-applied region in a forward or reverse direction along the second axis by calculating similarity or dissimilarity for clustering within a clustering range as wide as the segment along the second axis based on a respective reference value set for each clustering range; and
  - displaying the results according to a predetermined display format.
2. (Previously Presented) A method for displaying gene expression patterns according to claim 1, further comprising comparing a plurality of expression patterns of every two different genes to determine whether said genes are identical or not.
3. (Previously Presented) A method for displaying gene expression patterns according to claim 1, wherein some of the multiple genes have the same expression pattern at the beginning of said experiment cases but change to different expression patterns within the clustering-applied region along the second axis.
4. (Previously Presented) A method for displaying gene expression patterns according to claim 1, wherein some of the multiple genes have different expression patterns at the beginning of said experiment case but change to the same expression pattern within the clustering-applied region along the second axis.
5. (Previously Presented) A method for displaying gene expression patterns according to claim 1, wherein the experiment cases are conducted in a time sequence.

6. (Previously Presented) A method for displaying gene expression patterns according to claim 1, wherein the experiment cases are states of an individual's tissue.
7. (Re-instated) A method for displaying gene expression pattern according to claim 1, wherein the experiment cases are species of individuals.
8. (Re-instated & Currently Amended) A method for displaying gene expression pattern according to claim 1, wherein the experiment cases are ~~individual's sites~~ organ or tissue systems.
9. (Re-instated & Currently Amended) A method for displaying gene expression pattern according to claim 1, wherein the experiment cases are ~~presence and absence of an artificial condition~~ before and after drug administration.
10. (Re-instated & Currently Amended) A method for displaying gene expression pattern according to claim 1, wherein the experiment cases are a combination of time sequential experiments, states of individual's tissue, species of individuals, ~~individual's sites~~ organ or tissue systems, and ~~presence and absence of an artificial condition~~ before and after drug administration.
11. (Previously Presented) An apparatus for analyzing gene expression patterns, which acquires, from a database, expression pattern data of multiple genes whose expressions change according to experiment cases, where a first axis represents the genes and a second axis represents gene expression status of the experiment cases, the apparatus comprising:
  - an inputting means for designating a clustering-applied region along the second axis and a segment shorter than a width of the clustering-applied region along the second axis obtained from the database, and
  - an arithmetic unit for incrementally clustering the expression pattern data by the segment within the clustering-applied region in a forward or reverse direction along the second axis by calculating similarity or dissimilarity for clustering within a clustering range as wide as the segment along the second axis based on a respective reference value set for each clustering range; and

a display for displaying the results according to a predetermined display format.

12. (Withdrawn) A method for visually displaying expression patterns of multiple genes, comprising a step of displaying a round number of the cluster groups for each clustering phase taking a recognition error range in consideration, for the results of the clustering analysis of the gene expression pattern data.
13. (Withdrawn) A method for displaying expression patterns of multiple genes according to claim 12, wherein the results of the clustering analysis are displayed such that only clusters including a predetermined or greater number of the gene expression pattern data are displayed as a gene group.
14. (Withdrawn) An apparatus for displaying expression patterns of multiple genes, comprising:
  - a storage medium for storing expression pattern data of the genes;
  - an analysis processor for reading out the stored pattern data of genes for clustering analysis; and
  - a display processor for displaying a round number of the cluster groups for each clustering phase on a display screen taking a recognition error range in consideration, for the results of the analysis.
15. (Withdrawn) A storage medium for storing an operational program for visually displaying expression patterns of multiple genes on a display screen, wherein the stored operational program comprises a step of displaying the round number of the cluster groups for each clustering phase taking a recognition error range in consideration, for the results of the clustering analysis of the gene expression pattern data.
16. (Original) A method for displaying gene expression patterns according to claim 2:
  - wherein some of the multiple genes have the same expression pattern at the beginning of said experiment cases but change to different expression patterns within the clustering-applied region along the second axis.

17. (Original) A method for displaying gene expression patterns according to claim 2:  
wherein some of the multiple genes have different expression patterns at the beginning of said experiment case but change to the same expression pattern within the clustering-applied region along the second axis.